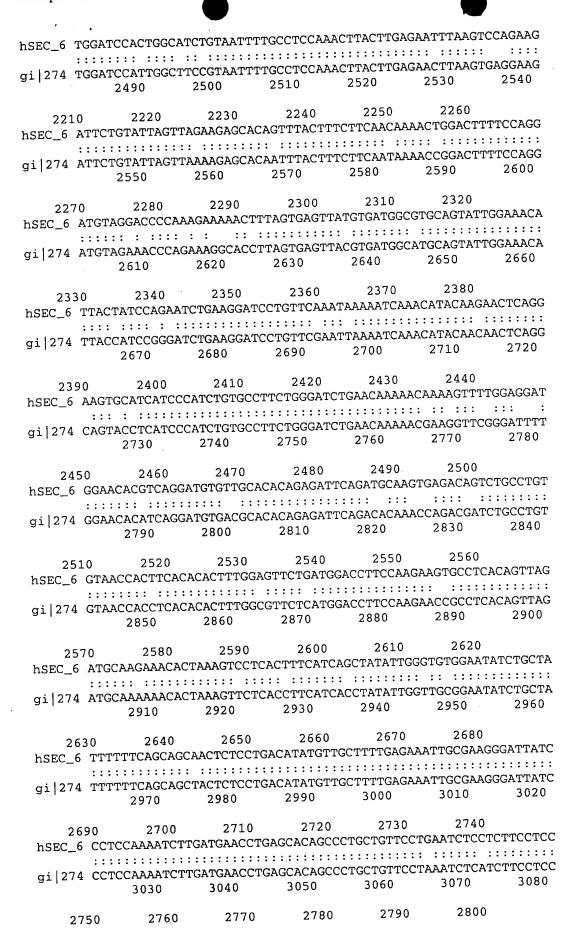
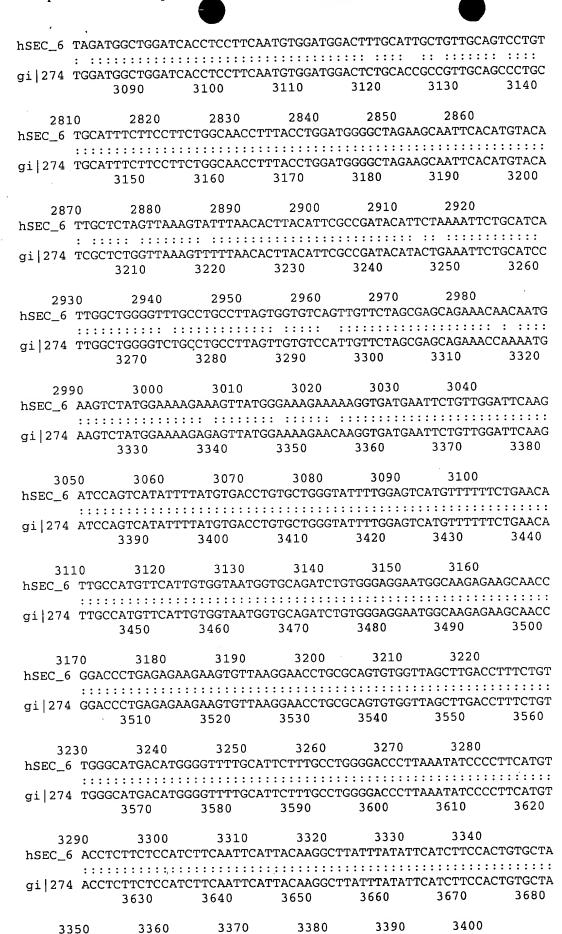
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FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448
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FASTA (3.34 January 2000) function [optimized, +5/-4 matrix (5:-4)] ktup: 6
 join: 91, opt: 76, gap-pen: -16/ -4, width: 16
 Scan time: 0.116
The best scores are:
gi|27435854|gb|AF216967.1| Homo sapiens putati (4550) [f] 11374
gi 27435854 gb AF216967.1 Homo sapiens putati (4550) [r]
>>gi|27435854|gb|AF216967.1| Homo sapiens putative vascu
 initn: 11373 init1: 11373 opt: 11374
 94.317% identity in 2534 nt overlap (1220-3753:1552-4085)
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                                                  1580
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          1530
                                            1300
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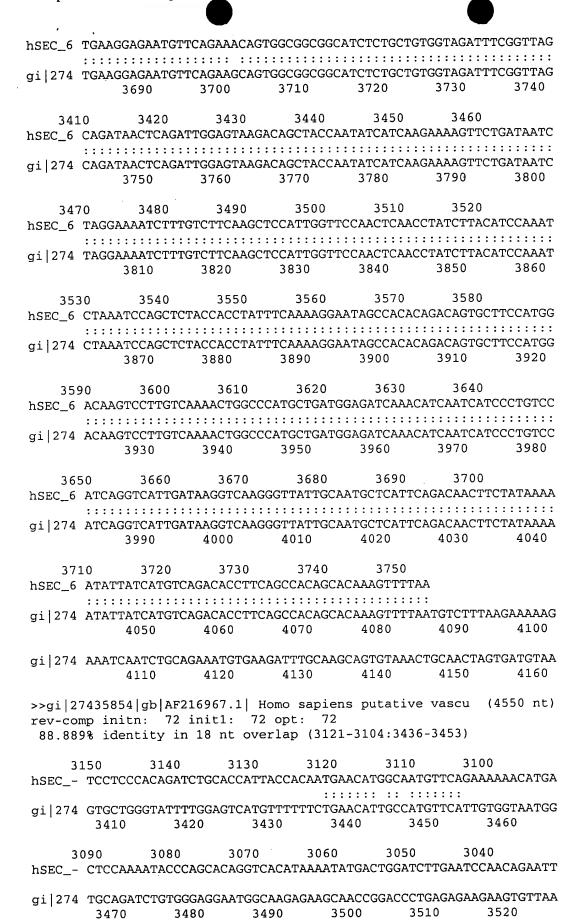


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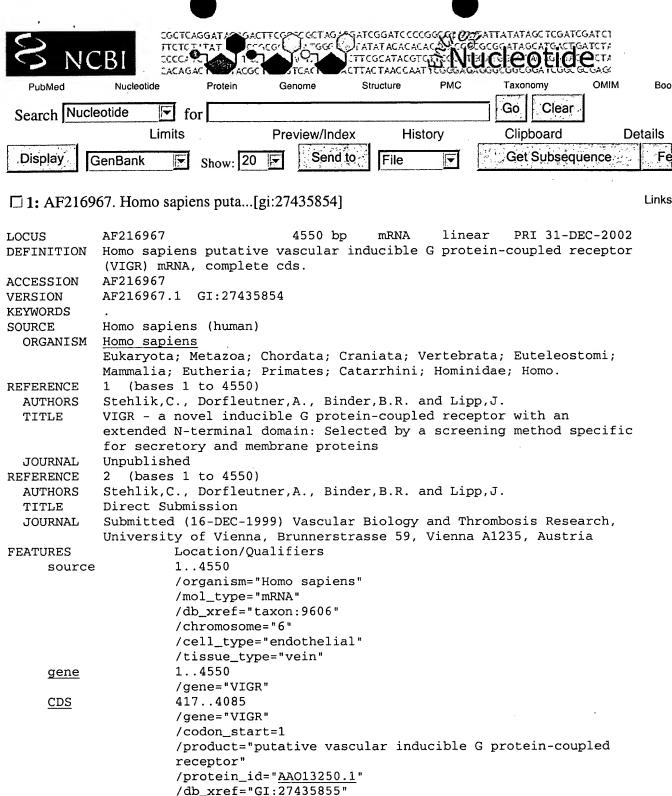


3753 residues in 1 query sequences 4550 residues in 1 library sequences Scomplib [version 3.3t05 March 30, 2000]

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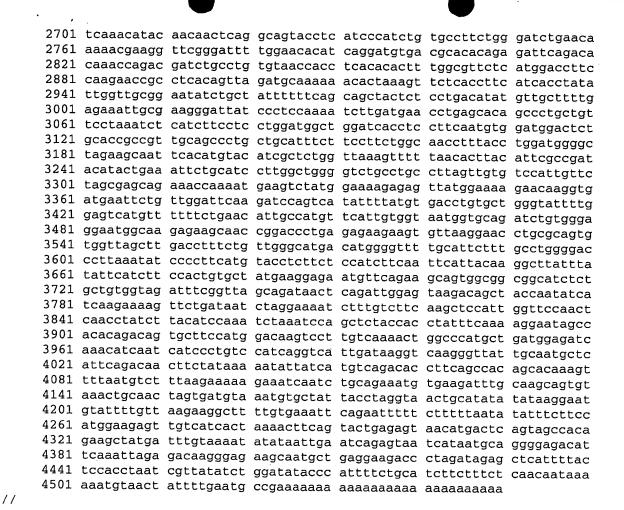
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Aug 6 2003 13:17:41